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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 00:17:03 ; Search time 2426.96 Seconds  
(without alignments) 10930.628 Million cell updates/sec

Title: US-09-001-737-7\_COPY\_15\_1652  
Perfect score: 1638 Sequence: ATGCCAAGAAATCAATT.....TGGCTGGATGCCGATAA 1638

Scoring table: IDENTITY\_NUC Gapop 10.0 , Gapext 1.0  
Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132  
Minimum DB seq length: 0 Maximum Match 0%  
Maximum DB seq length: 2000000000 Post-processing: Minimum Match 100%  
Listing first 45 summaries

Database : EST:  
1: em\_lestba: \*  
2: em\_leethun: \*  
3: em\_leetlin: \*  
4: em\_leestmu: \*  
5: em\_leetrov: \*  
6: em\_leatpi: \*  
7: em\_leetro: \*  
8: em\_lehcc: \*  
9: qb\_lestl: \*  
10: qb\_est2: \*  
11: qb\_htc: \*  
12: qb\_est3: \*  
13: qb\_est4: \*  
14: qb\_est5: \*  
15: em\_eston: \*  
16: em\_estfun: \*  
17: qb\_gss: \*  
18: em\_gss\_hum: \*  
19: em\_gss\_inv: \*  
20: em\_gss\_pln: \*  
21: em\_gss\_vit: \*  
22: em\_gss\_tun: \*  
23: em\_gss\_mam: \*  
24: em\_gss\_mus: \*  
25: em\_gss\_other: \*  
26: em\_gss\_pro: \*  
em\_gss\_rnd: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Length	DB ID	Description
1	471.8	28.8	2265	11 AY109623
2	431.4	26.3	2290	11 AY104969
3	430.6	26.3	2338	11 AY103778
4	414.2	25.3	1327	17 BH70613
5	383.8	23.4	2143	11 AY108560
6	302.8	18.5	1376	11 AY106465

SUMMARIES

REFERENCE	AUTHORS	TITLE	JOURNAL
Coe, E.C.		Direct Submission	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
FEATURES		Source	Location/Qualifiers
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			/organism="Zea mays"
			/db_xref="MaizeDB:30867"
			/db_xref="taxon:4577"
			/clone=CL2221_1"

ALIGNMENTS

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AUTHORS Coe, E.C.  
TITLE Direct Submission JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA

AY108518 Zea mays AY108518 clone Ba0 A428572 clone Ba0 BM99822 AGECOURT BF275584 GA\_EB002 AL518632 AL518632 AL53223 AL53223 B632193 zmo4\_0590 AL515622 AL515622 AL515579 AL515579 B196411 EST00862 BI026411 EST046300 BEF27437 HVSHB000 AL557150 AL557150 BI003174 OGG51F17 AL557181 AL557181 BQ967621 OHBUG09 AW224051 EST00862 BI014013 OGJD07 Y D46005 LCS1372A AW223768 EST00579 BI458421 AGECOURT AW223768 EST00579 BI000548 OGCG16B24 BI000548 AGECOURT AW223768 EST00579 BI458421 AGECOURT AW330455 PFOAFC33 BI518310 EST09221 EST077934 AJ432272 AJ432272 BQ599254 EST04154 BE22296 HWMM22Cf B221655 AGECOURT B888239 AGECOURT AI466765 EST24498 BQ915279 OHBUG423 BI176450 EST017749 BI176156 EST017749 BI354884 MBTSMLA13

/clone\_1.lib="Maize Mapping Project/DuPont Cornusensus Library"; this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

BASE COUNT	ORIGIN	615 a	430 c	599 g	538 t	83 others
<b>Query Match</b> 28.8%; Score 471.8; DB 11; Length 2265; Best Local Similarity 56.4%; Pred. No. 1.7e-120; Matches 911; Conservative 0; Mismatches 694; Indels 9; Gaps 3;						
QY	4	GCRANAGAATCCTAAATTTCAGCAGTGCAGCGCTCTGCCA	RGTGCGGAGTTGATC	63		
Db	293	GGAGAGGACATCAGTTGGTGTGAGCCCGCTGCTGAT	352			
QY	64	TTCAGCAGATACCTCAAACTAACGACTTGCTGCTAAGGCGCA	AGTGTGTTGAA	123		
Db	353	NNNNAGATGCTGCTCAAAGGACATGGCGCTTAAGGGCA	ATGTGCTGAA	412		
QY	124	GCTTGGTCTCCCTTAATCTAATGACGGGTAACTATGCTA	AGAGATGCTGAA	183		
Db	413	ACCTTGGGACCGAACGAACTACAGAAGGTTGACTGTA	GTGACAAAGCAT	472		
QY	184	GAAGATCATTTGAAACATGGGCAAAATTGTTGCTGAGTGC	TCTAAACCAAT	243		
Db	473	AGGGATAGTAGTAAGAATGATGTTGGCAGCTTGTAACAT	AT	532		
QY	244	GATATGCGGGGAGGGAGACTACTGCAACAGTTGACAC	CTTAAAGAATGCA	303		
Db	533	GCACATGCGGGGATGTTACAGTGGCAGCTTGTGAG	TTGAGCTTAA	592		
QY	304	GGACTAAAGATGTCACAGGTGTAACCAATTGTA	CCCTCGAGGATG	363		
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QY	364	GCACAGCACAGCTTGTGAGCCATTGACCTGTCAC	TTGAGCTTAA	423		
Db	653	GCTGTGAGCGTGTGACCACCTCTGAAAGGCTGCGCAG	ATGCAAGGAA	712		
QY	424	GCTATGTCAGGTGCTCACTACAGCTGCTGAA	--AATGTTGAG	480		
Db	713	GAATGTCAGGTGTTGCAATCTAGCAAAATGGGAA	AGGGAATGTT	772		
QY	481	TCAGAGCTATGGAGCGTGGCCACGATGTTTACCGT	GTGCTCTGCTAA	600		
Db	773	GCCAGGTATGAGGTTGCAAAAGGGTGTCATCA	TAATGCTACCC	832		
QY	541	ATTCAGACAGACTGCACTGTTGAGGATCATTGAC	CTTAAACGAA	1		
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QY	601	TACATGGCAGAACGAAATGAAAGGTTGCGAC	TGTAACCTTATCTATC	660		
Db	893	TACTCTTACCAACTCAAAGGCCAGAATGTTGAGA	GGACCCATGCTTA	952		
QY	661	ACGGATTAAGATGCTAACACATCAGCATTTCCACT	TTGGGAGTCTAA	720		
Db	953	CATGACAGAACGGTTAGCATGTTGCTGTTAGG	ATGAGTGCCTG	1012		
QY	721	ACCAACCTCTTACATCTTATGAGTGTGTTAGG	TTGAGATGCTG	780		
Db	1013	AAACAAAAGCTCTTACATCTTACATCTTACATCTT	AGTGTGCTG	1072		
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LOCUS	AY104969	AY104969	2290 bp	mRNA	linear	HTC 25-MAY-2002
DEFINITION	Zea mays	PCC070942	mRNA	sequence.		
ACCESSION	AY104969	AY104969				
VERSION	AY104969.1	AY104969.1	GI:21208047			
KEYWORDS	HTC.					
SOURCE	Zea mays.					
ORGANISM	Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; PACB clade; Panicoideae; Andropogoneae; Zea.					
REFERENCE	(bases 1 to 220)					
AUTHORS	Hainey, C.F., Bolan, M., Mao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanley, M., Morgan, M. and Tingey, S.V.					
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes					
JOURNAL	Unpublished (2002)					
REFERENCE	(bases 1 to 220)					
AUTHORS	Coe, E.C.					
TITLE	Direct Submission					
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of					

FEATURES	Missouri, Columbia, MO 65211, USA
source	Location/Qualifiers
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/db_xref="MGI:zebB:633867"	/db_xref="MGI:zebB:633867"
/clone="PC07042"	/clone="PC07042"
Library	Library
/note="this sequence is part of a project of EST assemblies resulting from the application public contigs to seed Dupont contigs; this resource was assembled by dupont as part of a collaboration with the overgo addressing of BACs in conjunction with the Maize Mapping Project."	/note="this sequence is part of a project of EST assemblies resulting from the application public contigs to seed Dupont contigs; this resource was assembled by dupont as part of a collaboration with the overgo addressing of BACs in conjunction with the Maize Mapping Project."
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Query Match	Query Match
Best Local Similarity	26.3%
Score	4314
DB	DB
Pred. No.	3-6e-109
Mismatches	57.9%
Conservative	522
Indels	19
Gaps	6
Query	52 GAGATGATATTAGCAGATACCGCAAGTACCGCTCCPAAAGGCCAATGCT 111
Db	426 GGGCACACAGCTCGAGCTCGTGGGGTTCTCTGGAC 485
Query	112 GAGCTTGAAAGACTGTTGCTTCTTAATTTCTAATGAGGGTAACTTCTATA 171
Db	486 GTCCTCGAGAACGAACTGCTACCTAAATTCATGTTGTCAGCTGGCAAG 545
Query	172 GAGATGATTTGAGATATTGTAAACAGATGGGACAAATGGTCTGAGCTGGT 231
Db	546 GAGGTGAATCTGAGACCTGAGCTTGAATATGGTCTGAGCTGGT 605
Query	232 TCTAAACCACTGATATTGCTGATGGAGGACTACTGCACAGTTGACAGCC 291
Db	606 GCTAAAGAACAAAGTACCTGGCTGGTGTGGACACACCCTGGTTCTCAAGCG 665
Query	292 ATGTTCTGAGGGACTAAATATGACAGCAGCTCTAATCCATGGPATCGTGA 351
Db	666 ATGTTACTGAGGTTTANAGGTGAGCTCTGGTCAATCCATGTCAGTCCTGGT 725
Query	352 GCGATTTGAAACGCAACGACAGCTGGTGAACCTGAAAGCCATGCTCACTTA 411
Db	726 GGTAATTGAGAACAGCCAACTGAGCTGGTGAACCTGCAATGGTCAAGGAGG 785
Query	412 TCTGGCAGGAGGACTTGTAGCTGGCTGGCAGTACATCACCTCT-GAAAGT 468
Db	786 TGAGCAGCTGGC-TTGCTGAGTGGCTGGCAGTTGCGGAAAPACTATGAA 843
Query	469 GAGAGTATCTCGAGACTATGGACGGCTGGCAGCTGGTGTGATACATCGA 528
Db	844 GGGATATGATGCTGGCTGGTGAAGAAGTGGGGCGAGATGTCATCTTAA 903
Query	529 GAACTCTGAGGATGAAACAGBACTGTGAGTGTGAAAGCTGCAATTGACCGTGT 588
Db	904 GAAGGAGAGGAGCTGCTGAAATACCTCTATTCTGTGAGGATGCACTTGGC 963
Query	589 TACCTGTTCTCATACATGCTCAGCAGCAGTAAATGGTCAAGCTGAAACCCA 648
Db	964 TATTTTCTGCCACTTGTGCTGAGCTGAAATGAGCTGCACTTGGTCC 1023
Query	649 TTATCTCATACACGATAAAGTGTCAACCTCAAGACATTGGCTTCACTTG 708
Db	1024 AAGCTCTCTGCTGGCTGGAGCAACATTAATGCGCAGACATCTACCTGG 1083
Query	709 GAGCTCTAAACCAACGCCATRACTCATTTGAGCTGGTGTGAGTGTGAGA 768
Db	1084 GATGCTTATGAGCTGGATGATCCAACTCTATGAGCTGAGCAAGGAACT 1143
Query	769 CTTCGAAACCTGCTGGTGTGAGCTGGATCTGGCTACTTCATGCTGGCTCAAAGC 828
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LOCUS	AY103778
DEFINITION	Zea mays mRNA sequence.
VERSION	AY103778
KEYWORDS	AY103778.1 GI:31206856
SOURCE	Zea mays
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
REFERENCE	1 (bases 1 to 2338)
AUTHORS	Hainey, C. F., Dolan, M., Miao, G. H., Vogel, J. M., Whitsitt, M. S., Arthur, L. W., Hausey, M., Morgante, M. and Tingey, S. V.
TITLE	Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes
JOURNAL	Unpublished (2002)
REFERENCE	2 (bases 1 to 2338)
QY	829 CCAGGATTTGGATGCTGTAAGCTTCTGAGACATGCTTCTGAGCTGCT 888
Db	1204 CCTGGTTTGGAGGCCAAACTCATCTATCTGATGACCTGCTACTGGGCC 1263
QY	889 ACAGTGATACAGAGTATCTAGGATTAAGATGAGCTAATGTTGAGGTGCTGAGCT 1008
Db	1264 ACTGTCATCAGAGAGTATGGATTCTTAGACAGCAGAGACAATGCGCTCTAGA 1323
QY	949 CAGGTGCTGATRACTGTGATAGCTGAACTGATGAACTATGTTGAGGTGCTGAGCT 1383
Db	1324 ACTGCTGTAAAGTGTCTTCTACAGGATCTCACACACATAGTGGGAGGACTACA 1443
QY	1009 TCAGAGCTATGCTAACGGTATGCACTATTAATGCTGATGAAACACAACACTCT 1128
Db	1384 CAGGAGGAGGAGAACGAAAGGGAGCACAAATGAGACAGTGTGACGAC 1503
QY	1069 GACTTGGCCGTTGAAACTACAGACAGCTGAGCTTAAAGAATGAGCTAACACTCT 1108
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QY	1129 ATCAATGGAGGCTCCACAGAGAGCTTAAGAATGAGACTCGCATTGAGGT 1188
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Db	.1524 CTTGTGAGGCTGTCATCAAAGTTGTGCAATATGAGGACCTGCGCAAGCT 1683
QY	1303 AC---TGGCGTACATTGCTCTGCTCTAGAAGAGCCTGACGCTGCAATGCTTA 1359
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QY	1360 ATGCTGGTGGAGGGCCCTAGCTATGAGAAG---TTGAAACACGCCCTGAGG 1415
Db	1744 ATGCGGGTAAATGCGAGCTGGTGTGAGTTGAGGAGTTCTGCACTGAGCTCG 1803
QY	1416 AACAGGTTTATGCTGACAGGGAGGTTGAGTTGATATTAAACAGGAACTATG 1475
Db	.1804 TATGGG-TACATGGCCACAGGGAGGTTGAGGACTTGTGCTGTGTCATGCA 1862
QY	1476 CCCTGTCAGAACACGATCACGCTACAGGCTTAAATGCGCTCTGAGCT 1535
Db	1863 TCCCACCAAGCTGGAGGCTGGCTGAGCATGCTGCACTGGGAAACCTCAT 1922
QY	1536 GACACGAGGAGCTGTTGCTAA 1559
Db	1923 CACCTCTGATGCTGGTTGTTGA 1946

AUTHORS	Coe, E.C.
TITLE	Direct Submission
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
FEATURES	Location/Qualifiers
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/clone_id="1b-Maize Mapping Project/DuPont Cornsensus Library"	
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ORIGIN	a 483 c 643 g 544 t
Query Match	26.3%
Best Local Similarity	56.2%
Matches	875
Conservative	0;
Mismatches	669;
Indels	13;
Gaps	3;
QY	52 GGAGTGATGATGTTAGCAGATACCGCAAGTAGCTTGTCTTAAAGGGCATAT 111
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Db	512 GTTGGAGGAGAAGTACCGCCTCCAAAGATGTTACGTTGGGGTACACTTCAAGA 571
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QY	232 TCTAAACCATGATATGGTGTGATGGACGACTCTGGACAACTTGTGAACTC 291
Db	632 GCTAAGAACGACGATCTTCTSGAGTGGACACACACCCTGGTCAGGG 691
QY	292 ATGTTCTGAGGAGCTAAATGACGAGGCTATCCAAATGGTATCCGTTGA 351
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QY	352 GGCAATGAAACGACGACAGCACAGGTTGAAAGCCATGCTCAACCTTA 411
Db	752 GGATCGKAAACAGCGAAAGCATGGTACATGGTAAAGCTACCGGAATGTT 811
QY	412 TCTGCCAAGGAGGAACTTCTCAGGPGCGCGTACCTCACCTCACCTGAA 471
Db	812 GAAATGAGTGGCTGCGATGTGTGATGTGTGATGTGTGCAACACTATGAAATGGT 871
QY	472 GAGTATCTAGAAGCTATGGAGCTGGCTGGGGAAACATGGTGTGATGAA 531
Db	872 AACATGATGAGGAGCATGGCATGGCAAGGGTGTACCTGTGAGAG 931
QY	532 TCTCGAGGATGAGAACAGACAGTGGTGAAGGCATGGTGTGATGAA 591
Db	932 GGAGGAGGTTCTGAGACHTCTCTAGTGTGGAGGAGTGCATTGTAC 991
QY	592 CTGCTCTACATAGTGACAGACATGAAATGATGCAAGCTGAAACCCATT 651
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QY	652 ATCTTAATCAGGAGATAAACATGCAACATCGAACAGATTGGCAC-TACTGAGGA 710
Db	1052 CTGCTTGGTGTGACAAAGATCACAAGCAGGGATCTPCTACGTTGAAGA 1111
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LOCUS	BH77013
DEFINITION	1327 bp DNA linear
	GSS 01-MAY-2002
ORGANISM	Lactococcus lactis subsp. cremoris
BACTERIA	Firmicutes; Lactobacillales; Streptococceae;
REFERENCE	1 (bases 1 to 137)
AUTHORS	Boletina, S.D. and Sorokin, A.
JOURNAL	Studies of genomes of dairy bacteria Lactococcus lactis SCI. Aliments, (2002) In press





	SOURCE	Zea mays.
	ORGANISM	Zea mays.
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Db	203 ACCCTCTTATTCTTATCCATGACAAACAAATCTCAACATGATCTCTTCACCAT	REFERENCE 1 (bases 1 to 1387)
OY	704 TTGGGAGAGCTTAAACACACCGCCATACTATCATATGCGATGATGTTGATGTG 763	AHaley,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morante,M. and Tingeay,S.V.
Db	263 TAGAATTCCTTCAGAATCGGAAGCTCTTCATGTCATGAGATTTGAGAG 322	TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Oligo Probes
OY	764 AAGCACTTCCAAACCTTGCTGCTGACAGATTCGGTACTTCATGCGATGATGTTGATGTG 763	JOURNAL Unpublished (2002)
Db	323 ATGCCTCTTCAGTCATGTTGACTGACAGATTCGGTCTTCATGTCATGAGATTTGAGAG 322	REFERENCE 2 (bases 1 to 1387)
OY	824 AGGCCAGAGATTTGCTGCGTAACGTTGACTGACAGATTCGGTCTTCATGTCATGAGATTTGAGAG 883	AUTHORS Arthur,L.W., Hanafey,M., Morante,M. and Tingeay,S.V.
Db	383 AAGCCTCCGTGAAATTGGGACATCTAGATGACATGCTGATGCTGATGCTG 442	TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Oligo Probes
OY	884 GTGGPACAGTGTTCAGGGATCTAGACTGATGATAAGATGCTCACATGAGAGCC 943	JOURNAL Unpublished (2002)
Db	443 GAGGAGAGTTTACGGAGGACGGGCTTGTGATCTGCGAACAGTCATGTCATGTCAG 502	REFERENCE 2 (bases 1 to 1387)
OY	944 TTGACAGGCTCTAGATAGTTGATGAAAGTAGACAGAGATGAGATGAGATGAGCTGAG 1003	AUTHORS Arthur,E.C.
Db	503 TTGGCACTGCTAAAGGTACTGTTCTCTTGTGATGATCTGATGATGATGATGATG 562	TITLE Direct Submission
OY	1004 CAACTTCGAAGCTTGTGTTACCGTATGCACTGACTGATGTTAAATGCAATGAAACCAA 1063	JOURNAL Submitted (25-MAR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65111, USA
Db	563 GTGACAAACAGGAGTAGTGTGAGGTTGCCAAGCACTGATGAGATGATGATGACAA 622	FEATURES Source
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OY	1124 CTGTTATGAAAGTAGGAGCTGACAGAGACCTTAAAGAAATTAACCTGGCTG 1183	/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize
Db	683 CTGACTCTAACATGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 742	BASE COUNT 426 a 257 c 372 g 332 t
OY	1184 AGGATGCTCTAAATCTACCTGCGCCGCTGAGAGGTATGTTGCTGCTGCTGCTG 1243	Matched 593; Similarity 56.0%; Pred. No. 1 to 59; Mismatches 455; Indels 10; Gaps 2;
Db	743 CAGATGCTCTAAATGCTGCAAGGCGCTGCTGCTGCTGCTGCTGCTG 802	Best_local_Similarity Conservative 0; Mismatches 455; Indels 10; Gaps 2;
OY	1244 CAGCACTTATGACGTTATGAAAGTAGCTGAGCTTGTGCTG -- AGGGCTATG 1300	Matches 593; Conservative 0; Mismatches 455; Indels 10; Gaps 2;
Db	803 TTGCCTCTTATGCTCACCAGGAGCTGCTGAGCTGAGCTGAGCTGAGCTG 862	Db 14 TGTGATGTTGAGGAGATGGAGATGCGCCGGTATATTCGCCACATTTGACAA 73
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Db	863 AGATGGAGTCAATTATCAGAACTCTGAGCTCTGAGCTGAGCTGAGCTG 922	Db 74 ACTCTGAGAAATATGTTGGAGTTGAGTTGAGTTGAGTTTAAACCAACCGTCAT 73
OY	1361 ATGGTGGTAGGAGCTGGCTGAGTATGACAGTGA--AAAAGCCCTGAGAA 1417	OY 674 TGTGACATCCAGACATTGCACTCTGAGGAGTTCTAAGGCTGATGCTGCAAT 733
Db	923 ATGGTGGCATGAGGAGCTATGATGCTGAGCTGAGCTGAGCTGAGCTG 982	Db 863 TCAAGGATGAAAGGAAATCTCCGCTTGGAGAACACAGCTGAGCCCTC 133
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Db	983 TGGCTATGAGCAGCAAAGGGAGTAGCTGAGCATGATGTCAGGCCATCATCCATC 1042	Db 194 TGTCTATATGCTGAGGACATCTACTGCTGAGCTTGCACACTCTGTGTTAACAGC 253
OY	1478 CTGCGAAAGTACACGATCACGGCTTACAGCTCTGAGCTGAGCTTCAAC 1537	OY 794 TTGGTGTACTTCATGTTGCTGCTCTCAAGGCGCCGAGTTGGTGTCTGTAAG 853
Db	1043 CGCGAAGGTGATCGACCCGCTCACAGGAGCTGCTGTTCTGATGCGAA 1102	Db 254 TGGAGGAACTTCATGTTGCGCTGAGCTTGGCTGAGCTTGGCTGAGCTG 313
OY	1538 CAACAGAGCTGTTGCTTAACTAACCTGAAAC 1571	OY 854 CTATGTTGAGACATGCTATGCTGAGCTGAGCTGTTGAGCTGAGCTGAGCTG 913
Db	1103 CAACGGAGGCCCTCTCGAGCTCCCGCAC 1136	Db 314 CTTGACTTCAGGAGCTGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 373
RESULT 7		OY 914 TGGATTAAGAGTCTACATGAGCCGCTGGAGACGCTCTGAGATTAAGGTTGATA 973
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DEFINITION	sea mays PC0123570 mRNA sequence.	OY 974 ATGATGCGACGATTTGAGGTCGAGGTCGAGCTGAGCTGAGCTGAGCTGAGCTG 1033
ACCESSION	AY108518	Db 434 ACTCTGACACCCCTATGCGATGCGACCTAACAGATGAGATGCGAGGAGATG 493
KEYWORDS	AY108518.1 GI:21211596 HPC.	Db 494 CTTGACTGAGAGGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 553



RESULT 9  
 Db 625 TTTATGCCGCGCTAATCTGGTAAAGGTGAAACCTTGACTTATGAGT 684  
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 NIH-MGC http://mgc.ncbi.nlm.nih.gov/  
 AUTHOR National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Tissue Procurement: NCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNUU)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNUU at:  
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RESULT 10  
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 SOURCE Gossypium arboreum.  
 ORGANISM Gossypium arboreum.  
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 REFERENCE 1 (uses 1 to 878)  
 AUTHORS King, R.K., Frisch, D., Yu, Y., Main, D., Rambo, T.R., Simmons, J., Henry, D., Wood, T.C., Leslie, A., and Wilkins, T.A.  
 TITLE An integrated analysis of the genetics, development, and evolution  
 of the cotton fiber  
 Unpublished (2000)



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 vector. Library was normalized. Library was constructed  
 by Life Technologies. Contact: Feng Liang Life  
 Technologies, a division of Invitrogen 9800 Medical Center  
 Drive Rockville, Maryland 20850, USA Fax: (+1) 301 610  
 8371 Email: fliang@lifetech.com URL:  
<http://fulllength.invitrogen.com>"  
 1 others

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RESULT 12

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VERSION	AL532233.1	GI:12795726
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SOURCE		
ORGANISM		
Bukai,Yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
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REFERENCE	1 (bases 1 to 988)	
AUTHORS	L.J.W.B., Gruber,C., Jeesee,J. and Polayes,D.	
TITLE	Full-length cDNA libraries and normalization	
JOURNAL	unpublished (2001)	
COMMENT	Contact: Genoscope	
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